

APPENDIX

- Original SEQ ID NOS 1-3 remain the same;
- Original SEQ ID NOS 4-6 are now SEQ ID NOS 4-5, 6-7 & 8-9, respectively;
- Original SEQ ID NO: 7 is now SEQ ID NO:10;
- Original SEQ ID NO: 8 is now SEQ ID NO:11;
- Original SEQ ID NO: 9 is now SEQ ID NO:12;
- Original SEQ ID NO: 10 is now SEQ ID NO:13;

***Please note that the part or all of the CDS regions for original SEQ ID NOS 8-10 were either incorrect or contained internal stop codons; since the amino acids were not explicitly listed in application, these coding regions were left out of the corrected Sequence Listing.**

- Original SEQ ID NO: 11 is now SEQ ID NOS 14-15;
- Original SEQ ID NO: 12 is now SEQ ID NOS 16-17;
- Original SEQ ID NO: 13 is now SEQ ID NOS 18-19;
- Original SEQ ID NO: 14 is now SEQ ID NOS 20-21;
- Original SEQ ID NOS 15-17 are now SEQ ID NOS 22-24;
- Original SEQ ID NOS 18-19 are now SEQ ID NOS 25-26 & 27-28, respectively;
- Original SEQ ID NO: 20 is now SEQ ID NO:29;

***See above note re: SEQ ID NOS 8-10.**

- Original SEQ ID NOS 21-22 are now SEQ ID NOS 30-31 & 32-33, respectively;
- Original SEQ ID NO: 23 is now SEQ ID NO:34;

***See above note re: SEQ ID NOS 8-10.**

- Original SEQ ID NO: 24 is now SEQ ID NO:35;
- Original SEQ ID NO: 25 is now SEQ ID NOS 36-37;

***See above note re: SEQ ID NOS 8-10.**

- Original SEQ ID NO: 26 is now SEQ ID NO:38;

***See above note re: SEQ ID NOS 8-10.**

- Table 1 encompasses SEQ ID NO:39;
- Table 3 encompasses SEQ ID NO:40;
- Table 4 encompasses SEQ ID NOS 24, 35 & 41-45, respectively.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Yokoi, Haruhiko
Shiotsu, Yukimasa
Konishi, Noboru
- (ii) TITLE OF INVENTION: NOVEL POLYPEPTIDES
- (iii) NUMBER OF SEQUENCES: 45
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: NIXON & VANDERHYE P.C.
 - (B) STREET: 1100 North Glebe Rd. 8th floor
 - (C) CITY: Arlington
 - (D) STATE: VA
 - (E) COUNTRY: USA
 - (F) ZIP: 22201-4741
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/765,337
 - (B) FILING DATE: 23-DEC-1996
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/JP96/01157
 - (B) FILING DATE: 26-APR-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP P.HEI.7-102625
 - (B) FILING DATE: 26-APR-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Crawford, Arthur R.
 - (B) REGISTRATION NUMBER: 25,327
 - (C) REFERENCE/DOCKET NUMBER: 249-89
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 703-816-4000
 - (B) TELEFAX: 703-816-4100

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 328 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu
1 5 10 15
Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val
20 25 30
His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu
35 40 45
Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu
50 55 60
Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln
65 70 75 80
Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln
85 90 95
Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu
100 105 110
Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe
115 120 125
Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
130 135 140
Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Thr Tyr Arg Ala
145 150 155 160
Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg
165 170 175
Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr
180 185 190
Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu
195 200 205
Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln
210 215 220
Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln
225 230 235 240
Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
245 250 255
Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
260 265 270
Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln
275 280 285
Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly
290 295 300

Val Leu Val Ser His Leu Gln Ser Phe Leu G Val Ser Tyr Arg
 305 310 315 320

Val Leu Arg His Leu Ala Gln Pro
 325

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu
 1 5 10 15

Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val
 20 25 30

His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu
 35 40 45

Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu
 50 55 60

Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln
 65 70 75 80

Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln
 85 90 95

Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu
 100 105 110

Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe
 115 120 125

Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
 130 135 140

Val Gly Gly Ser Thr Leu Cys Val Arg Gly Gly Gly Ser Gly Gly Gly
 145 150 155 160

Ser Gly Gly Gly Ser Arg Ala Pro Thr Tyr Arg Ala Ser Ser Leu Pro
 165 170 175

Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly
 180 185 190

Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys
 195 200 205

His Pro Glu Leu Val Leu Leu Gly His Ser Gly Ile Pro Trp
 210 215 220
 Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys
 225 230 235 240
 Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln
 245 250 255
 Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu
 260 265 270
 Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu
 275 280 285
 Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro
 290 295 300
 Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala
 305 310 315 320
 Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His
 325 330 335
 Leu Ala Gln Pro
 340

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 344 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu
 1 5 10 15
 Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val
 20 25 30
 His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu
 35 40 45
 Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu
 50 55 60
 Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln
 65 70 75 80
 Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln
 85 90 95
 Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu
 100 105 110

Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	115	120	125
Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	130	135	140
Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Ser	Gly	Gly	Gly	Ser	Gly	Gly	145	150	155
Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Arg	Ala	Pro	Thr	Tyr	Arg	Ala	165	170	175
Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	180	185	190
Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	195	200	205
Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	210	215	220
Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	225	230	235
Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	245	250	255
Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	260	265	270
Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	275	280	285
Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	290	295	300
Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	305	310	315
Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	325	330	335
Val	Leu	Arg	His	Leu	Ala	Gln	Pro									340		

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1047 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 1..63

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 64..1047

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG GAG CTG ACT GAA TTG CTC CTC GTG GTC ATG CTT CTC CTA ACT GCA	48
Met Glu Leu Thr Glu Leu Leu Val Val Met Leu Leu Leu Thr Ala	
-21 -20 -15 -10	
AGG CTA ACG CTG TCC AGC CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC	96
Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val	
-5 1 5 10	
CTC AGT AAA CTG CTT CGT GAC TCC CAT GTC CTT CAC AGC AGA CTG AGC	144
Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser	
15 20 25	
CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT GTC CTG CTG CCT GCT	192
Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala	
30 35 40	
GTG GAC TTT AGC TTG GGA GAA TGG AAA ACC CAG ATG GAG GAG ACC AAG	240
Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys	
45 50 55	
GCA CAG GAC ATT CTG GGA GCA GTG ACC CTT CTG CTG GAG GGA GTG ATG	288
Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met	
60 65 70 75	
GCA GCA CGG GGA CAA CTG GGA CCC ACT TGC CTC TCA TCC CTC CTG GGG	336
Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly	
80 85 90	
CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT GGG GCC CTG CAG AGC CTC	384
Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu	
95 100 105	
CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG ACC ACA GCT CAC AAG GAT	432
Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp	
110 115 120	
CCC AAT GCC ATC TTC CTG AGC TTC CAA CAC CTG CTC CGA GGA AAG GTG	480
Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val	
125 130 135	
CGT TTC CTG ATG CTT GTA GGA GGG TCC ACC CTC TGC GTA CGG CGG GCG	528
Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala	
140 145 150 155	
CCA ACA TAT CGC GCC TCG AGT CTA CCA CAG AGC TTC CTT TTA AAA AGC	576
Pro Thr Tyr Arg Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser	
160 165 170	

TTA GAG CAA GTG	175	AAG ATC CAG GGC GAT GGC GCA G	180	TC CAG GAG	185	624
Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala				Leu Gln Glu		
AAG CTG TGT GCC ACC TAC AAG CTG TGC CAC CCC GAG GAG CTG GTG CTG	190	195	200			672
Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu						
CTC GGA CAC TCT CTG GGC ATC CCC TGG GCT CCC CTG AGC AGC TGC CCC	205	210	215			720
Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro						
AGC CAG GCC CTG CAG CTG GCA GGC TGC TTG AGC CAA CTC CAT AGC GGC	220	225	230			768
Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly						
CTT TTC CTC TAC CAG GGG CTC CTG CAG GCC CTG GAA GGG ATC TCC CCC	240	245	250			816
Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro						
GAG TTG GGT CCC ACC TTG GAC ACA CTG CAG CTG GAC GTC GCC GAC TTT	255	260	265			864
Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe						
GCC ACC ACC ATC TGG CAG CAG ATG GAA GAA CTG GGA ATG GCC CCT GCC	270	275	280			912
Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala						
CTG CAG CCC ACC CAG GGT GCC ATG CCG GCC TTC GCC TCT GCT TTC CAG	285	290	295			960
Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln						
CGC CGG GCA GGA GGG GTC CTA GTT GCC TCC CAT CTG CAG AGC TTC CTG	300	305	310			1008
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu						
GAG GTG TCG TAC CGC GTT CTA CGC CAC CTT GCC CAG CCC	320	325				1047
Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro						

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Leu Thr Glu Leu Leu Val Val Met Leu Leu Leu Thr Ala		
-21 -20	-15	-10
Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val		
-5	1	5
		10
Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser		
15	20	25

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 1..63

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 64..1083

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG GAG CTG ACT GAA TTG CTC CTC GTG GTC ATG CTT CTC CTA ACT GCA	48
Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala	
-21 -20 -15 -10	
AGG CTA ACG CTG TCC AGC CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC	96
Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val	
-5 1 5 10	
CTC AGT AAA CTG CTT CGT GAC TCC CAT GTC CTT CAC AGC AGA CTG AGC	144
Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser	
15 20 25	
CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT GTC CTG CTG CCT GCT	192
Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala	
30 35 40	
GTG GAC TTT AGC TTG GGA GAA TGG AAA ACC CAG ATG GAG GAG ACC AAG	240
Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys	
45 50 55	
GCA CAG GAC ATT CTG GGA GCA GTG ACC CTT CTG CTG GAG GGA GTG ATG	288
Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met	
60 65 70 75	
GCA GCA CGG GGA CAA CTG GGA CCC ACT TGC CTC TCA TCC CTC CTG GGG	336
Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly	
80 85 90	
CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT GGG GCC CTG CAG AGC CTC	384
Gln Leu Ser Gly Gln Val Arg Leu Leu Gly Ala Leu Gln Ser Leu	
95 100 105	
CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG ACC ACA GCT CAC AAG GAT	432
Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp	
110 115 120	

CCC Pro 125	AAT Asn	GCC Ala	ATC Ile	TTC Phe	CTG Leu	AGC Ser	TTC Phe	CAA Gln	CAC His	CTG Leu	CTC Leu	CGA Arg	GGA Gly	AAG Lys	GTG Val	480
CGT Arg 140	TTC Phe	CTG Leu	ATG Met	CTT Leu	GTA Val	GGA Gly	GGG Gly	TCC Ser	ACC Thr	CTC Leu	TGC Cys	GTC Val	AGG Arg	GGT Gly	GGC Gly	528
GGT Gly	TCT Ser	GGA Gly	GGT Gly	GGT Gly	TCC Ser	GGA Gly	GGG Gly	GGT Gly	TCT Ser	AGA Arg	GCA Ala	CCA Pro	ACA Thr	TAT Tyr	CGC Arg	576
GCC Ala	TCG Ser	AGT Ser	CTA Leu	CCA Pro	CAG Gln	AGC Ser	TTC Phe	CTT Leu	TTA Leu	AAA Lys	AGC Ser	TTA Leu	GAG Glu	CAA Gln	GTG Val	624
AGG Arg	AAG Lys	ATC Ile	CAG Gln	GGC Gly	GAT Asp	GGC Gly	GCA Ala	GCG Ala	CTC Leu	CAG Gln	GAG Glu	AAG Lys	CTG Leu	TGT Cys	GCC Ala	672
ACC Thr	TAC Tyr	AAG Lys	CTG Leu	TGC Cys	CAC His	CCC Pro	GAG Glu	GAG Glu	CTG Leu	GTG Val	CTG Leu	CTC Leu	GGA Gly	CAC His	TCT Ser	720
CTG Leu 220	GGC Gly	ATC Ile	CCC Pro	TGG Trp	GCT Ala	CCC Pro	CTG Leu	AGC Ser	AGC Ser	TGC Cys	CCC Pro	AGC Ser	CAG Gln	GCC Ala	CTG Leu	768
CAG Gln	CTG Leu	GCA Ala	GGC Gly	TGC Cys	TTG Leu	AGC Ser	CAA Gln	CTC Leu	CAT His	AGC Ser	GGC Gly	CTT Leu	TTC Phe	CTC Leu	TAC Tyr	816
CAG Gln	GGG Gly	CTC Leu	CTG Leu	CAG Gln	GCC Ala	CTG Leu	GAA Glu	GGG Gly	ATC Ile	TCC Ser	CCC Pro	GAG Glu	TTG Leu	GGT Gly	CCC Pro	864
ACC Thr	TTG Leu	GAC Asp	ACA Thr	CTG Leu	CAG Gln	CTG Leu	GAC Asp	GTC Val	GCC Ala	GAC Asp	TTT Phe	GCC Ala	ACC Thr	ACC Thr	ATC Ile	912
TGG Trp 285	CAG Gln	CAG Gln	ATG Met	GAA Glu	GAA Glu	CTG Leu	GGA Gly	ATG Met	GCC Ala	CCT Pro	GCC Ala	CTG Leu	CAG Gln	CCC Pro	ACC Thr	960
CAG Gln 300	GGT Gly	GCC Ala	ATG Met	CCG Pro	GCC Ala	TTC Phe	GCC Ala	TCT Ser	GCT Ala	TTC Phe	CAG Gln	CGC Arg	CGG Arg	GCA Ala	GGA Gly	1008
GGG Gly	GTC Val	CTA Leu	GTT Val	GCC Ala	TCC Ser	CAT His	CTG Leu	CAG Gln	AGC Ser	TTC Phe	CTG Leu	GAG Glu	GTG Val	TCG Ser	TAC Tyr	1056
CGC Arg	GTT Val	CTA Leu	CGC Arg	CAC His	CTT Leu	GCC Ala	CAG Gln	CCC Pro								1083

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 amino acids

(B) E: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala
-21 -20 -15 -10
Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val
-5 1 5 10
Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser
15 20 25
Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala
30 35 40
Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys
45 50 55
Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met
60 65 70 75
Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly
80 85 90
Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu
95 100 105
Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp
110 115 120
Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val
125 130 135
Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Gly Gly
140 145 150 155
Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Arg Ala Pro Thr Tyr Arg
160 165 170
Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
175 180 185
Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala
190 195 200
Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser
205 210 215
Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu
220 225 230 235
Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr
240 245 250
Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro
255 260 265

GCA GCA CGG GGA CAA CTG GGA CCC ACT TGC CTC TCA TCC CTC CTG GGG Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly	336
80 85 90	
CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT GGG GCC CTG CAG AGC CTC Gln Leu Ser Gly Gln Val Arg Leu Leu Gly Ala Leu Gln Ser Leu	384
95 100 105	
CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG ACC ACA GCT CAC AAG GAT Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp	432
110 115 120	
CCC AAT GCC ATC TTC CTG AGC TTC CAA CAC CTG CTC CGA GGA AAG GTG Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val	480
125 130 135	
CGT TTC CTG ATG CTT GTA GGA GGG TCC ACC CTC TGC GTA CGG TCC GGA Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Ser Gly	528
140 145 150 155	
GGT GGC TCT GGC GGT GGT TCT GGT GGC GGC TCC GGA GGC GGT CGT GCG Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Arg Ala	576
160 165 170	
CCA ACA TAT CGC GCC TCG AGT CTA CCA CAG AGC TTC CTT TTA AAA AGC Pro Thr Tyr Arg Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser	624
175 180 185	
TTA GAG CAA GTG AGG AAG ATC CAG GGC GAT GGC GCA GCG CTC CAG GAG Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu	672
190 195 200	
AAG CTG TGT GCC ACC TAC AAG CTG TGC CAC CCC GAG GAG CTG GTG CTG Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu	720
205 210 215	
CTC GGA CAC TCT CTG GGC ATC CCC TGG GCT CCC CTG AGC AGC TGC CCC Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro	768
220 225 230 235	
AGC CAG GCC CTG CAG CTG GCA GGC TGC TTG AGC CAA CTC CAT AGC GGC Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly	816
240 245 250	
CTT TTC CTC TAC CAG GGG CTC CTG CAG GCC CTG GAA GGG ATC TCC CCC Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro	864
255 260 265	
GAG TTG GGT CCC ACC TTG GAC ACA CTG CAG CTG GAC GTC GCC GAC TTT Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe	912
270 275 280	
GCC ACC ACC ATC TGG CAG CAG ATG GAA GAA CTG GGA ATG GCC CCT GCC Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala	960
285 290 295	
CTG CAG CCC ACC CAG GGT GCC ATG CCG GCC TTC GCC TCT GCT TTC CAG Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln	1008
300 305 310 315	

CGC CGG GCA GGA GGG GTC CTA GTT GCC TCC CAT CTG CAG AGC TTC CTG 1056
 Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu
 320 325 330

GAG GTG TCG TAC CGC GTT CTA CGC CAC CTT GCC CAG CCC 1095
 Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
 335 340

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala
 -21 -20 -15 -10
 Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val
 -5 1 5 10
 Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser
 15 20 25
 Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala
 30 35 40
 Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys
 45 50 55
 Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met
 60 65 70 75
 Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly
 80 85 90
 Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu
 95 100 105
 Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp
 110 115 120
 Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val
 125 130 135
 Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Ser Gly
 140 145 150 155
 Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Arg Ala
 160 165 170
 Pro Thr Tyr Arg Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser
 175 180 185
 Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
 190 195 200

Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
 205 210 215
 Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro
 220 225 230 235
 Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly
 240 245 250
 Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro
 255 260 265
 Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe
 270 275 280
 Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala
 285 290 295
 Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
 300 305 310 315
 Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu
 320 325 330
 Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
 335 340

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 27..44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTCTCCAAGC TTGAATTC CG GCCAGAATGG AGCTGACTGA ATTG

44

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTAGAGGTAC CGCGGCCGCT TACCCTTCCT GAGACAGATT CTGGGAG

47

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGAACCTCTG GGCCTGGCT CAGT

24

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCTGCCTGCT GTGGACTTTA GCTT

24

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGT TGG AAG CTC AAG ATG GCA
Cys Trp Lys Leu Arg Lys Met Ala
1 5

24

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys Trp Lys Leu Arg Lys Met Ala
1 5

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCT GAT GCT TGT AGG AGG GTC CAC
Pro Asp Ala Cys Arg Arg Val His
1 5

24

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Asp Ala Cys Arg Arg Val His
1 5

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TCA AGA GTT CGT GTA TCC TGT TCA
Ser Arg Val Arg Val Ser Cys Ser
1 5

24

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ser Arg Val Arg Val Ser Cys Ser
1 5

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAA TGG AAC TCG TGG ACT CTT TCC
Glu Trp Asn Ser Trp Thr Leu Ser
1 5

24

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Glu Trp Asn Ser Trp Thr Leu Ser
1 5

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTAAAACGAC GGCCAGT

17

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAGGAAACAG CTATGAC

17

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE RIPTION: SEQ ID NO:24:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(1..3, 43..66)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGC TCTAGAACCG CCTCCGGAAC CACCTCCAGA ACCGCCACC CCT GAC GCA GAG	54
Cys Pro Asp Ala Glu	
1 5	
GGT GGA CCC TCC	66
Gly Gly Pro Ser	

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys Pro Asp Ala Glu Gly Gly Pro Ser
1 5

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 22..45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGTTCCGGAG GCGGTTCTAG A GCA CCA ACA TAT CGC GCC TCG AGT
Ala Pro Thr Tyr Arg Ala Ser Ser
1 5

45

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ala Pro Thr Tyr Arg Ala Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CATTCCGCGG GGTACCGCGG CCGCTCAGGG CTGGGCAAGG TGGCGTAG

48

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGC TGC TTG AGC CAA CTC CAT AGC
Gly Cys Leu Ser Gln Leu His Ser
1 5

24

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Gly Cys Leu Ser Gln Leu His Ser
1 5

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GAC CCA ACT CGG GGG AGA TCC CTT
Asp Pro Thr Arg Gly Arg Ser Leu
1 5

24

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Asp Pro Thr Arg Gly Arg Ser Leu
1 5

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (ix) FEATURE:
 - (A) NAME/KEY: mutation
 - (B) LOCATION: replace(25, "")

- (ix) FEATURE:
 - (A) NAME/KEY: mutation
 - (B) LOCATION: replace(33..34, "")

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TAGACTCGAG GCGCGATATG TTGGCGCCCG CCGTACGCAG AGGGTGGACC CTCCTAC

57

- (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
 1 5 10 15

Arg

- (2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..6

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 7..57

(D) OTHER INFORMATION: /product= "linker peptide"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..5

(D) OTHER INFORMATION: /product= "SplI"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 7..12

(D) OTHER INFORMATION: /product= "MroI"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 43..48

(D) OTHER INFORMATION: /product= "MroI"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 58..61

(D) OTHER INFORMATION: /product= "BbeI"

(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(4..5, "")

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTA CGG TCCGGAGGTG GCTCTGGCGG TGGTTCTGGT GGCGGCTCCG GAGGCGGTCCG

56

Val Arg

1

TGCGC

61

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Val Arg

1

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..51
 (D) OTHER INFORMATION: /product= "linker peptide"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 53
 (D) OTHER INFORMATION: /product= "SplI"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 10..15
 (D) OTHER INFORMATION: /product= "MroI"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 46..51
 (D) OTHER INFORMATION: /product= "MroI"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ACGACCGCCT CCGGAGCCGC CACCAGAACC ACCGCCAGAG CCACCTCCGG ACC

53

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 175 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Xaa Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1 5 10 15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
 20 25 30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Gly Leu
 35 40 45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
 50 55 60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
 65 70 75 80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
 85 90 95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
 100 105 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
115 120 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
130 135 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145 150 155 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170 175

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu
1 5 10 15

Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val
20 25 30

His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu
35 40 45

Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu
50 55 60

Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln
65 70 75 80

Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln
85 90 95

Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu
100 105 110

Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe
115 120 125

Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
130 135 140

Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr Ala
145 150 155 160

Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu Pro Asn
165 170 175

Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr
 180 185 190
 Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile
 195 200 205
 Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly
 210 215 220
 Tyr Leu Asn Arg Ile His Glu Leu Leu Asn Gly Thr Arg Gly Leu Phe
 225 230 235 240
 Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro Asp Ile Ser Ser Gly
 245 250 255
 Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly Tyr Ser
 260 265 270
 Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu Phe Pro Leu
 275 280 285
 Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu His Pro Leu Leu Pro
 290 295 300
 Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr
 305 310 315 320
 Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu Gly
 325 330

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ser Gly Gly Gly Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser Gly Gly Gly
1

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Gly Gly Gly Ser Gly Gly Gly Ser
1 5